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searching Seq2 library
 Comparison of:
(A) Seq1        >Seq1    (540 nucleotides)      SEQ ID NO:1            - 540 nt
(B) Seq2        >Seq2    (540 nucleotides)      SEQ ID NO:3            - 540 nt
using matrix file DNA

  99.3% identity in 540 nt overlap; init: 2132, opt: 2132

            10        20        30        40        50        60
Seq1  ATGCCGATCGAGTACAAGCCTGAAATCCAGCACTCCGATTTCAAGGACCTGACCAACCTG
      X:::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Seq2  ATGCCGATCAAGTACAAGCCTGAAATCCAGCACTCCGATTTCAAGGACCTGACCAACCTG
            10        20        30        40        50        60


            70        80        90       100       110       120
Seq1  ATCCACTTCCAGAGCATGGAAGGCAAGATCTGGCTTGGCGAACAGCGCATGCTGTTGCTG
      :::::::::::::::::::::::::::::::::::::::::::::::: :::::::::::::::
Seq2  ATCCACTTCCAGAGCATGGAAGGCAAGATCTGGCTTGGCGAACAACGCATGCTGTTGCTG
            70        80        90       100       110       120


           130       140       150       160       170       180
Seq1  CAGTCTTCAGCGATGGCCAGCTTTCGCCGGGAAATGGTCAATACCCTGGGCATCGAACGC
      ::::: :::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Seq2  CAGTTTTCAGCGATGGCCAGCTTTCGCCGGGAAATGGTCAATACCCTGGGCATCGAACGC
           130       140       150       160       170       180


           190       200       210       220       230       240
Seq1  GCCAAGGGCTTGTTCCTGCGCCATGGTTACCAGTCCGGCCTGAAGGATGCCGAACTGGCC
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Seq2  GCCAAGGGCTTGTTCCTGCGCCATGGTTACCAGTCCGGCCTGAAGGATGCCGAACTGGCC
           190       200       210       220       230       240


           250       260       270       280       290       300
Seq1  AGGAAGCTGAGACCGAATGCCAGCGAAGTCGGCATGTTCCTCGCTGGGCCGCAGATGCAT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Seq2  AGGAAGCTGAGACCGAATGCCAGCGAAGTCGGCATGTTCCTCGCTGGGCCGCAGATGCAT
           250       260       270       280       290       300


           310       320       330       340       350       360
Seq1  TCACTCAAGGGTCTGGTCAAGGTCCGCCCCACCGAGCTCGATATCGACAAGGAATACGGG
      :::::::::::::::::::::::::::::::::::: :::::::::::::::::::::::::::
Seq2  TCACTCAAGGGTCTGGTCAAGGTCCGCCCCACCGGGCTCGATATCGACAAGGAATACGGG
           310       320       330       340       350       360


           370       380       390       400       410       420
Seq1  CGCTTCTATGCCGAGATGGAGTGGATCGACTGGTTCGAGGTGGAAATCTGCCAGACCGAC
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Seq2  CGCTTCTATGCCGAGATGGAGTGGATCGACTGGTTCGAGGTGGAAATCTGCCAGACCGAC
           370       380       390       400       410       420


           430       440       450       460       470       480
Seq1  CTGGGGCAGATGCAAGACCCGGTGTGCTGGACTGTGCTCGGCTACGCCTGCGCCTATTCC
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Seq2  CTGGGGCAGATGCAAGACCCGGTGTGCTGGACTGTGCTCGGCTACGCCTGCGCCTATTCC
           430       440       450       460       470       480


           490       500       510       520       530       540
Seq1  TCGGCGTTCATGGGCCGGGAAATCATCTTCAAGGAAGTCAGCTGCCGCGGCTGCGGCGGC
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::X
Seq2  TCGGCGTTCATGGGCCGGGAAATCATCTTCAAGGAAGTCAGCTGCCGCGGCTGCGGCGGC
           490       500       510       520       530       540

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   54.5% identity in 55 nt overlap; init:    40, opt:    45


             490        500        510        520        530
Seq1    GGCGTTCATGGGCCGGGAAATCATCTTCAAGGAAGTCAGCTGCCGCGGCTGCGGC
        :::     : :   X:::::::::X  ::    :       : ::     :::: :     :::
Seq2    GGCCAGCTTTCGCCGGGAAATGGTCAATACCCTGGGCATCGAACGCGCCAAGGGC
             140        150        160        170        180
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   52.7% identity in 110 nt overlap; init:    40, opt:    49


              90         100        110        120        130
Seq1    AGGCAAGATCTGGCTTGGCGAACAGCGC-ATGCTGTTGCTGCAGTCTTCAGCGATGGCCA
        : :::::::: : ::   ::   : :: : ::    :::     ::::    : :    :    :::
Seq2    ATGCAAGACCCGGTGTGCTGGACTGTGCTCGGCTACGCCTGC--GCCTATTCCTCGGCGT
         430        440         450    460        470        480


        140        150        160        170        180
Seq1    GCTTTCGCCGGGAAATGGTCAATACCCTGGGCATCGAACGCGCCAAGGGC
        : : :    X:::::::::X  ::    :       : :: :     :::: :     :::
Seq2    TCATGGGCCGGGAAATCATCTTCAAGGAAGTCAGCTGCCGCGGCTGCGGC
         490        500        510        520        530
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